Figure 1A

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                                     M   Q   R   L   G   A   T   L   L   C     10
 GGCACGAGGGGGCGGCGGCTGCGGGCGCAGAGCGGAG ATG CAG CGG CTT GGG GCC ACC CTG CTG TGC     67

 L   L   L   A   A   A   V   P   T   A   P   A   P   A   P   T   A   T   S   A     30
CTG CTG CTG GCG GCG GCG GTC CCC ACG GCC CCC GCG CCC GCT CCG ACG GCG ACC TCG GCT    127

 P   V   K   P   G   P   A   L   S   Y   P   Q   E   E   A   T   L   N   E   M     50
CCA GTC AAG CCC GGC CCG GCT CTC AGC TAC CCG CAG GAG GAG GCC ACC CTC AAT GAG ATG    187

 F   R   E   V   E   E   L   M   E   D   T   Q   H   K   L   R   S   A   V   E     70
TTC CGC GAG GTT GAG GAA CTG ATG GAG GAC ACG CAG CAC AAA TTG CGC AGC GCG GTG GAA    247

 E   M   E   A   E   E   A   A   A   K   A   S   S   E   V   N   L   A   N   L     90
GAG ATG GAG GCA GAA GAA GCT GCT GCT AAA GCA TCA TCA GAA GTG AAC CTG GCA AAC TTA    307

 P   P   S   Y   H   N   E   T   N   T   D   T   K   V   G   N   N   T   I   H    110
CCT CCC AGC TAT CAC AAT GAG ACC AAC ACA GAC ACG AAG GTT GGA AAT AAT ACC ATC CAT    367

 V   H   R   E   I   H   K   I   T   N   N   Q   T   G   Q   M   V   F   S   E    130
GTG CAC CGA GAA ATT CAC AAG ATA ACC AAC AAC CAG ACT GGA CAA ATG GTC TTT TCA GAG    427

 T   V   I   T   S   V   G   D   E   E   G   R   R   S   H   E   C   I   I   D    150
ACA GTT ATC ACA TCT GTG GGA GAC GAA GAA GGC AGA AGG AGC CAC GAG TGC ATC ATC GAC    487

 E   D   C   G   P   S   M   Y   C   Q   F   A   S   F   Q   Y   T   C   Q   P    170
GAG GAC TGT GGG CCC AGC ATG TAC TGC CAG TTT GCC AGC TTC CAG TAC ACC TGC CAG CCA    547

 C   R   G   Q   R   M   L   C   T   R   D   S   E   C   C   G   D   Q   L   C    190
TGC CGG GGC CAG AGG ATG CTC TGC ACC CGG GAC AGT GAG TGC TGT GGA GAC CAG CTG TGT    607

 V   W   G   H   C   T   K   M   A   T   R   G   S   N   G   T   I   C   D   N    210
GTC TGG GGT CAC TGC ACC AAA ATG GCC ACC AGG GGC AGC AAT GGG ACC ATC TGT GAC AAC    667

 Q   R   D   C   Q   P   G   L   C   C   A   F   Q   R   G   L   L   F   P   V    230
CAG AGG GAC TGC CAG CCG GGG CTG TGC TGT GCC TTC CAG AGA GGC CTG CTG TTC CCT GTG    727

 C   T   P   L   P   V   E   G   E   L   C   H   D   P   A   S   R   L   L   D    250
TGC ACA CCC CTG CCC GTG GAG GGC GAG CTT TGC CAT GAC CCC GCC AGC CGG CTT CTG GAC    787

 L   I   T   W   E   L   E   P   D   G   A   L   D   R   C   P   C   A   S   G    270
CTC ATC ACC TGG GAG CTA GAG CCT GAT GGA GCC TTG GAC CGA TGC CCT TGT GCC AGT GGC    847

 L   L   C   Q   P   H   S   H   S   L   V   Y   V   C   K   P   T   F   V   G    290
CTC CTC TGC CAG CCC CAC AGC CAC AGC CTG GTG TAT GTG TGC AAG CCG ACC TTC GTG GGG    907

 S   R   D   Q   D   G   E   I   L   L   P   R   E   V   P   D   E   Y   E   V    310
AGC CGT GAC CAA GAT GGG GAG ATC CTG CTG CCC AGA GAG GTC CCC GAT GAG TAT GAA GTT    967

 G   S   F   M   E   E   V   R   Q   E   L   E   D   L   E   R   S   L   T   E    330
GGC AGC TTC ATG GAG GAG GTG CGC CAG GAG CTG GAG GAC CTG GAG AGG AGC CTG ACT GAA   1027

 E   M   A   L   G   E   P   A   A   A   A   A   A   L   L   G   G   E   E   I    350
GAG ATG GCG CTG GGG GAG CCT GCG GCT GCC GCC GCT GCA CTG CTG GGA GGG GAA GAG ATT   1087

 *                                                                                351
TAG                                                                              1090
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Figure 1B

ATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAAATAGCTAATTTATTTCCCCANGTGTGTGCTTTAAGCGTGGGCTG 1169

ACCAGGCTTCTTCCTACATCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTCAG 1248

CTCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAACTGCAGGAGCAGTTTGC 1327

CACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCGTTTGTTCTACATGGCTTTGATAATTG 1406

TTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTT 1485

TGCAAACATCAACCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCT 1564

TCAGCTGTTGCAGATGAAATGTTCTGTTCACCCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCCTAC 1643

CTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTC 1722

CTCGTCCATCAGGGATTTCAGAGGCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAG 1801

TTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCC 1880

AAAAGGAAGGAGAATGGGATTTTTCTTTTGAGGCATGCACATCTGGAATTAAGGTCAAACTAATTCTCACATCCCTCTA 1959

AAAGTAAACTACTGTTAGGAACAGCAGTGTTCTCACAGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGAC 2038

ACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAA 2117

CAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAACTGAAGACAATTATCA 2196

ACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACG 2275

CCACTCCACAAATGATGTTTTCAGGTGTCATGGACTGTTGCCACCATGTATTCATCCAGAGTTCTTAAAGTTTAAAGTT 2354

GCACATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGCATAA 2433

ATCACTTCAACTGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2479

Figure 2

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GAATTCGGCACGAGAGACGACGTGCTGAGCTGCCAGCTTAGTGGAAGCTCTGCTCTGGGTGGAGAGCAGCCTCGCTTTG   79

                                                        M   V   A   A   V   L   L   G      8
GTGACGCACAGTGCTGGGACCCTCCAGGAGCCCCGGGATTGAAGG ATG GTG GCG GCC GTC CTG CTG GGG    148

 L   S   W   L   C   S   P   L   G   A   L   V   L   D   F   N   N   I   R   S    28
CTG AGC TGG CTC TGC TCT CCC CTG GGA GCT CTG GTC CTG GAC TTC AAC AAC ATC AGG AGC   208

 S   A   D   L   H   G   A   R   K   G   S   Q   C   L   S   D   T   D   C   N    48
TCT GCT GAC CTG CAT GGG GCC CGG AAG GGC TCA CAG TGC CTG TCT GAC ACG GAC TGC AAT   268

 T   R   K   F   C   L   Q   P   R   D   E   K   P   F   C   A   T   C   R   G    68
ACC AGA AAG TTC TGC CTC CAG CCC CGC GAT GAG AAG CCG TTC TGT GCT ACA TGT CGT GGG   328

 L   R   R   R   C   Q   R   D   A   M   C   C   P   G   T   L   C   V   N   D    88
TTG CGG AGG AGG TGC CAG CGA GAT GCC ATG TGC TGC CCT GGG ACA CTC TGT GTG AAC GAT   388

 V   C   T   T   M   E   D   A   T   P   I   L   E   R   Q   L   D   E   Q   D   108
GTT TGT ACT ACG ATG GAA GAT GCA ACC CCA ATA TTA GAA AGG CAG CTT GAT GAG CAA GAT   448

 G   T   H   A   E   G   T   T   G   H   P   V   Q   E   N   Q   P   K   R   K   128
GGC ACA CAT GCA GAA GGA ACA ACT GGG CAC CCA GTC CAG GAA AAC CAA CCC AAA AGG AAG   508

 P   S   I   K   K   S   Q   G   R   K   G   Q   E   G   E   S   C   L   R   T   148
CCA AGT ATT AAG AAA TCA CAA GGC AGG AAG GGA CAA GAG GGA GAA AGT TGT CTG AGA ACT   568

 F   D   C   G   P   G   L   C   C   A   R   H   F   W   T   K   I   C   K   P   168
TTT GAC TGT GGC CCT GGA CTT TGC TGT GCT CGT CAT TTT TGG ACG AAA ATT TGT AAG CCA   628

 V   L   L   E   G   Q   V   C   S   R   R   G   H   K   D   T   A   Q   A   P   188
GTC CTT TTG GAG GGA CAG GTC TGC TCC AGA AGA GGG CAT AAA GAC ACT GCT CAA GCT CCA   688

 E   I   F   Q   R   C   D   C   G   P   G   L   L   C   R   S   Q   L   T   S   208
GAA ATC TTC CAG CGT TGC GAC TGT GGC CCT GGA CTA CTG TGT CGA AGC CAA TTG ACC AGC   748

 N   R   Q   H   A   R   L   R   V   C   Q   K   I   E   K   L   *               225
AAT CGG CAG CAT GCT CGA TTA AGA GTA TGC CAA AAA ATA GAA AAG CTA TAA               799

ATATTTCAAAATAAAGAAGAATCCACATTGCAAAAAAAAAAAAAAAAAA                                848
```

Figure 3

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GTCGACCCACGCGTCCGCGGACGCGTGGGCGGCACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTC 79

                              M   M   A   L   G   A   A   G   A   T   R   V    12
TTTCTTTCTCCCTCTTGAGTCCTTCTGAG ATG ATG GCT CTG GGC GCA GCG GGA GCT ACC CGG GTC  144

 F   V   A   M   V   A   A   A   L   G   G   H   P   L   L   G   V   S   A   T   32
TTT GTC GCG ATG GTA GCG GCG GCT CTC GGC GGC CAC CCT CTG CTG GGA GTG AGC GCC ACC 204

 L   N   S   V   L   N   S   N   A   I   K   N   L   P   P   P   L   G   G   A   52
TTG AAC TCG GTT CTC AAT TCC AAC GCT ATC AAG AAC CTG CCC CCA CCG CTG GGC GGC GCT 264

 A   G   H   P   G   S   A   V   S   A   A   P   G   I   L   Y   P   G   G   N   72
GCG GGG CAC CCA GGC TCT GCA GTC AGC GCC GCG CCG GGA ATC CTG TAC CCG GGC GGG AAT 324

 K   Y   Q   T   I   D   N   Y   Q   P   Y   P   C   A   E   D   E   E   C   G   92
AAG TAC CAG ACC ATT GAC AAC TAC CAG CCG TAC CCG TGC GCA GAG GAC GAG GAG TGC GGC 384

 T   D   E   Y   C   A   S   P   T   R   G   G   D   A   G   V   Q   I   C   L   112
ACT GAT GAG TAC TGC GCT AGT CCC ACC CGC GGA GGG GAC GCA GGC GTG CAA ATC TGT CTC 444

 A   C   R   K   R   R   K   R   C   M   R   H   A   M   C   C   P   G   N   Y   132
GCC TGC AGG AAG CGC CGA AAA CGC TGC ATG CGT CAC GCT ATG TGC TGC CCC GGG AAT TAC 504

 C   K   N   G   I   C   V   S   S   D   Q   N   H   F   R   G   E   I   E   E   152
TGC AAA AAT GGA ATA TGT GTG TCT TCT GAT CAA AAT CAT TTC CGA GGA GAA ATT GAG GAA 564

 T   I   T   E   S   F   G   N   D   H   S   T   L   D   G   Y   S   R   R   T   172
ACC ATC ACT GAA AGC TTT GGT AAT GAT CAT AGC ACC TTG GAT GGG TAT TCC AGA AGA ACC 624

 T   L   S   S   K   M   Y   H   T   K   G   Q   E   G   S   V   C   L   R   S   192
ACC TTG TCT TCA AAA ATG TAT CAC ACC AAA GGA CAA GAA GGT TCT GTT TGT CTC CGG TCA 684

 S   D   C   A   S   G   L   C   C   A   R   H   F   W   S   K   I   C   K   P   212
TCA GAC TGT GCC TCA GGA TTG TGT TGT GCT AGA CAC TTC TGG TCC AAG ATC TGT AAA CCT 744

 V   L   K   E   G   Q   V   C   T   K   H   R   R   K   G   S   H   G   L   E   232
GTC CTG AAA GAA GGT CAA GTG TGT ACC AAG CAT AGG AGA AAA GGC TCT CAT GGA CTA GAA 804

 I   F   Q   R   C   Y   C   G   E   G   L   S   C   R   I   Q   K   D   H   H   252
ATA TTC CAG CGT TGT TAC TGT GGA GAA GGT CTG TCT TGC CGG ATA CAG AAA GAT CAC CAT 864

 Q   A   S   N   S   S   R   L   H   T   C   Q   R   H   *    267
CAA GCC AGT AAT TCT TCT AGG CTT CAC ACT TGT CAG AGA CAC TAA 909

ACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACCTTTTATGACCTTCATCAACTCAATC 988

CTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCATTCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGT 1067

TTCTTTATGGAACTCCCCTGTGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAA 1146

TGAAACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTTGTTATGTAAATTTTTGTACACATTGAT 1225

TGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATTTCAGCTTATAGTTCTTAAAAGCATAACCCTT 1304

TACCCCATTTAATTCTAGAGTCTAGAACGCAAGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAA 1383

AATACTAGCTTATTTTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGAAAT 1462

AAAATTTAACATTTAATATCATGAAATGTTATAAGTAGACATAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 1536
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Figure 4A

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GTCGACCCACGCGTCCGGCGGGAGCCCGCGGCGAGCGTAGCGCAAGTCCGCTCCCTAGGCATCGCTGCGCTGGCAGCGA 79

TTCGCTGTCTCTTGTGAGTCAGGGGACAACGCTTCGGGGCAACTGTGAGTGCGCGTGTGGGGGACCTCGATTCTCTTCA 158

GATCTCGAGGATTCGGTCCGGGGACGTCTCCTGATCCCCTACTAAAGCGCCTGCTAACTTTGAAAAGGAGCACTGTGTC 237

CTGCAAAGTTTGACACATAAAGGATAGGAAAAGAGAGGAGAGAAAAGCAACTGAGTTGAAGGAGAAGGAGCTGATGCGG 316

GCCTCCTGATCAATTAAGAGGAGAGTTAAACCGCCGAGATCCCGGCGGGACCAAGGAGGTGCGGGGCAAGAAGGAACGG 395

AAGCGGTGCGATCCACAGGGCTGGGTTTTCTTGCACCTTGGGTCACGCCTCCTTGGCGAGAAAGCGCCTCGCATTTGAT 474

TGCTTCCAGTTATTGCAGAACTTCCTGTCCTGGTGGAGAAGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGG 553

CGTGAGACTGAGTTCATAGGGTCCTGGGTCCCCGAACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCGACC 632

CAAGTGAGGGGCCCCGTGTTGGGGTCCTCCCTCCCTTTGCATTCCCACCCCTCCGGGCTTTGCGTCTTCCTGGGGACCC 711

                M   A   A   L   M   R   S   K   D   S   S   C   C   L   L   L   L   17
CCTCGCCGGGAG ATG GCC GCG TTG ATG CGG AGC AAG GAT TCG TCC TGC TGC CTG CTC CTA CTG 774

 A   A   V   L   M   V   E   S   S   Q   I   G   S   S   R   A   K   L   N   S    37
GCC GCG GTG CTG ATG GTG GAG AGC TCA CAG ATC GGC AGT TCG CGG GCC AAA CTC AAC TCC  834

 I   K   S   S   L   G   G   E   T   P   G   Q   A   A   N   R   S   A   G   M    57
ATC AAG TCC TCT CTG GGC GGG GAG ACG CCT GGT CAG GCC GCC AAT CGA TCT GCG GGC ATG  894

 Y   Q   G   L   A   F   G   G   S   K   K   G   K   N   L   G   Q   A   Y   P    77
TAC CAA GGA CTG GCA TTC GGC GGC AGT AAG AAG GGC AAA AAC CTG GGG CAG GCC TAC CCT  954

 C   S   S   D   K   E   C   E   V   G   R   Y   C   H   S   P   H   Q   G   S    97
TGT AGC AGT GAT AAG GAG TGT GAA GTT GGG AGG TAT TGC CAC AGT CCC CAC CAA GGA TCA 1014

 S   A   C   M   V   C   R   R   K   K   K   R   C   H   R   D   G   M   C   C   117
TCG GCC TGC ATG GTG TGT CGG AGA AAA AAG AAG CGC TGC CAC CGA GAT GGC ATG TGC TGC 1074

 P   S   T   R   C   N   N   G   I   C   I   P   V   T   E   S   I   L   T   P   137
CCC AGT ACC CGC TGC AAT AAT GGC ATC TGT ATC CCA GTT ACT GAA AGC ATC TTA ACC CCT 1134

 H   I   P   A   L   D   G   T   R   H   R   D   R   N   H   G   H   Y   S   N   157
CAC ATC CCG GCT CTG GAT GGT ACT CGG CAC AGA GAT CGA AAC CAC GGT CAT TAC TCA AAC 1194

 H   D   L   G   W   Q   N   L   G   R   P   H   T   K   M   S   H   I   K   G   177
CAT GAC TTG GGA TGG CAG AAT CTA GGA AGA CCA CAC ACT AAG ATG TCA CAT ATA AAA GGG 1254

 H   E   G   D   P   C   L   R   S   S   D   C   I   E   G   F   C   C   A   R   197
CAT GAA GGA GAC CCC TGC CTA CGA TCA TCA GAC TGC ATT GAA GGG TTT TGC TGT GCT CGT 1314

 H   F   W   T   K   I   C   K   P   V   L   H   Q   G   E   V   C   T   K   Q   217
CAT TTC TGG ACC AAA ATC TGC AAA CCA GTG CTC CAT CAG GGG GAA GTC TGT ACC AAA CAA 1374

 R   K   K   G   S   H   G   L   E   I   F   Q   R   C   D   C   A   K   G   L   237
CGC AAG AAG GGT TCT CAT GGG CTG GAA ATT TTC CAG CGT TGC GAC TGT GCG AAG GGC CTG 1434

 S   C   K   V   W   K   D   A   T   Y   S   S   K   A   R   L   H   V   C   Q   257
TCT TGC AAA GTA TGG AAA GAT GCC ACC TAC TCC TCC AAA GCC AGA CTC CAT GTG TGT CAG 1494

 K   I   *   260
AAA ATT TGA 1503

TCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAGCATGGTGGAAAATAAGGTT 1582

CAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAAAAAGGGAGAAAGAAAACATGAAC 1661

TGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTTCCATTATGCAACTTGTCTATGTAAATAATGTACAC 1740
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Figure 4B

ATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATTACTGATGAGTAGCATGTGACTTTCCAAGAGT 1819
TTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGCTTATACAAATAACCTACATGCCAGATTTCTATTCA 1898
ACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTATACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAAT 1977
GAAAACATGGAGCATTGTTAATTTACAACAGAAAATTACCTTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAG 2056
TCTTGGTAGATAAGAAAAAAATCAGTCAATATTTCCAAATAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTA 2135
GGAAGACAAATAAATAACAAACAAACAGCCACAAATACTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAA 2214
CTGATACAAGACAAAAACAGTTCCTTCAGATTCTACGGAATGACAGTATATCTCTCTTTATCCTATGTGATTCCTGCTC 2293
TGAATGCATTATATTTTCCAAAGTATACCCATAAATTGTGACTAGTAAAATACTTACACAGAGCAGAATTTTCACAGAT 2372
GGCAAAAAAATTTAAAGATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCAT 2451
AACCTGTATTTTGATAGAATTAGATTGGTAAATACATGTATTCATACATACTCTGTGGTAATAGAGACTTGAGCTGGAT 2530
CTGTACTGCACTGGAGTAAGCAAGAAAATTGGGAAAACTTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATG 2609
TCTGAGGCACAAGTTGGCTGTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT 2688
CATAATNTTTCCTATGCNGNTGAATTCNGTGTGAGGTCCTGTGTCCGTCCTATCCTCAAATTATTTATTTTATAGTGCT 2767
GAGATCCTCAAATAATCTCAATTTCGGAGGTTTCACAAAATGGACTCCTGAAGTAGACAGAGTAGTGAGGTTTCATTGC 2846
CCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTCTTCCCAAACCTCTGCAGCATCTGCTTTATTGCCAAA 2925
GGGCTAGTTTCGGTTTTCTGCCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTAAAACCTGCATATTGCTAA 3004
TCTATAGACACCACAGTTTCTAAATTCTTTGAAACCACTTTACTACTTTTTTAAACTTAACTCAGTTCTAAATACTTT 3083
GTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTTGTGACTTTAAACTTTTGTAGACCACAATTCACTTTTTAGTT 3162
TTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCCAGTAGAGATTGAGTTTGAGCCTGTATATCTATT 3241
AAAAATTTCAACTTCCCACATATATTTACTAAGATGATTAAGACTTACATTTTCTGCACAGGTCTGCAAAAACAAAAAT 3320
TATAAACTAGTCCATCCAAGAACCAAAGTTTGTATAAACAGGTTGCTATAAGCTTGGTGAAATGAAAATGGAACATTTC 3399
AATCAAACATTTCCTATATAACAATTATTATATTTACAATTTGGTTTCTGCAATATTTTTCTTATGTCCACCCTTTTAA 3478
AAATTATTATTTGAAGTAATTTATTTACAGGAAATGTTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAG 3557
CTTTGTAGCAGAATATATTTGCAGCTATTGACTTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTT 3636
TTCTCCTCTAAAAACTGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC 3687

Figure 5A

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FGTCGACCCACGCGTCCGCTGTGGCAGCCCAGCTACCGGTCGTGACCAGATCCAGCTTGCAGCTCAGCTTTGTTCATTC   79

                               M   Q   R   L   G   G   I   L   L   C   T   L     12
GAATTGGGCGGCGGCCAGCGCGGAACAAAC ATG CAG CGG CTC GGG GGT ATT TTG CTG TGT ACA CTG   145

 L   A   A   A   V   P   T   A   P   A   P   S   P   T   V   T   W   T   P   A     32
CTG GCG GCG GCG GTC CCC ACT GCT CCT GCT CCT TCC CCG ACG GTC ACT TGG ACT CCG GCG   205

 E   P   G   P   A   L   N   Y   P   Q   E   E   A   T   L   N   E   M   F   R     52
GAG CCG GGC CCA GCT CTC AAC TAC CCT CAG GAG GAA GCT ACG CTC AAT GAG ATG TTT CGA   265

 E   V   E   E   L   M   E   D   T   Q   H   K   L   R   S   A   V   E   E   M     72
GAG GTG GAG GAG CTG ATG GAA GAC ACT CAG CAC AAA CTG CGC AGT GCC GTG GAG GAG ATG   325

 E   A   E   E   A   A   A   K   T   S   S   E   V   N   L   A   S   L   P   P     92
GAG GCG GAA GAA GCA GCT GCT AAA ACG TCC TCT GAG GTG AAC CTG GCA AGC TTA CCT CCC   385

 N   Y   H   N   E   T   S   T   E   T   R   V   G   N   N   T   V   H   V   H    112
AAC TAT CAC AAT GAG ACC AGC ACG GAG ACC AGG GTG GGA AAT AAC ACA GTC CAT GTG CAC   445

 Q   E   V   H   K   I   T   N   N   Q   S   G   Q   V   V   F   S   E   T   V    132
CAG GAA GTT CAC AAG ATA ACC AAC AAC CAG AGT GGA CAG GTG GTC TTT TCT GAG ACA GTC   505

 I   T   S   V   G   D   E   E   G   K   R   S   H   E   C   I   I   D   E   D    152
ATT ACA TCT GTA GGG GAT GAA GAA GGC AAG AGG AGC CAT GAA TGT ATC ATT GAT GAA GAC   565

 C   G   P   T   R   Y   C   Q   F   S   S   F   K   Y   T   C   Q   P   C   R    172
TGT GGG CCC ACC AGG TAC TGC CAG TTC TCC AGC TTC AAG TAC ACC TGC CAG CCA TGC CGG   625

 D   Q   Q   M   L   C   T   R   D   S   E   C   C   G   D   Q   L   C   A   W    192
GAC CAG CAG ATG CTA TGC ACC CGA GAC AGT GAG TGC TGT GGA GAC CAG CTG TGT GCC TGG   685

 G   H   C   T   Q   K   A   T   K   G   G   N   G   T   I   C   D   N   Q   R    212
GGT CAC TGC ACC CAA AAG GCC ACC AAA GGT GGC AAT GGG ACC ATC TGT GAC AAC CAG AGG   745

 D   C   Q   P   G   L   C   C   A   F   Q   R   G   L   L   F   P   V   C   T    232
GAT TGC CAG CCT GGC CTG TGT TGT GCC TTC CAA AGA GGC CTG CTG TTC CCC GTG TGC ACA   805

 P   L   P   V   E   G   E   L   C   H   D   P   T   S   Q   L   L   D   L   I    252
CCC CTG CCC GTG GAG GGA GAG CTC TGC CAT GAC CCC ACC AGC CAG CTG CTG GAT CTC ATC   865

 T   W   E   L   E   P   E   G   A   L   D   R   C   P   C   A   S   G   L   L    272
ACC TGG GAA CTG GAG CCT GAA GGA GCT TTG GAC CGA TGC CCC TGC GCC AGT GGC CTC CTA   925

 C   Q   P   H   S   H   S   L   V   Y   M   C   K   P   A   F   V   G   S   H    292
TGC CAG CCA CAC AGC CAC AGT CTG GTG TAC ATG TGC AAG CCA GCC TTC GTG GGC AGC CAT   985

 D   H   S   E   E   S   Q   L   P   R   E   A   P   D   E   Y   E   D   V   G    312
GAC CAC AGT GAG GAG AGC CAG CTG CCC AGG GAG GCC CCG GAT GAG TAC GAA GAT GTT GGC  1045

 F   I   G   E   V   R   Q   E   L   E   D   L   E   R   S   L   A   Q   E   M    332
TTC ATA GGG GAA GTG CGC CAG GAG CTG GAA GAC CTG GAG CGG AGC CTA GCC CAG GAG ATG  1105
```

Figure 5B

```
 A   F   E   G   P   A   P   V   E   S   L   G   G   E   E   E   I   *          350
GCA TTT GAG GGG CCT GCC CCT GTG GAG TCA CTA GGC GGA GAG GAG GAG ATT TAG         1159

GCCCAGACCCAGCTGAGTCACTGGTAGATGTGCAATAGAAATGGCTAATTTATTTTCCCAGGAGTGTCCCCAAGTGTGG 1238

AATGGCCGCAGCTCCTTCCCAGTAGCTTTTCCTCTGGCTTGACAAGGTACAGTGCAGTACATTTCTTCCAGCCGCCCTG 1317

CTTCTCTGACTTGGGAAAGACAGGCATGGCGGGTAAGGGCAGCGGTGAGTCGTCCCTCGCTGTTGCTAGAAACGCTGTC 1396

TTGTTCTTCATGGATGGAAGATTTGTTTGAAGGGAGAGGATGGGAAGGGGTGAAGTCTGCTCATGATGGATTTGGGGGA 1475

TACAGGGAGGAGGATGCCTGCCTTGCAGACGTGGACTTGGCAAAATGTAACCTTTGCTTTTGTCTTGCGCCGCTCCCAT 1554

GGGCTGAGGCAGTGGCTACACAAGAGCTATGCTGCTCTGTGGCCTCCCACATATTCATCCCTGTGTTTCAGCTCCTACC 1633

TCACTGTCAGCACAGCCCTTCATAGCCACGCCCCCTCTTGCTCACCACAGCCTAGGAGGGGACCAGAGGGGACTTCTCT 1712

CAGAGCCCCATGCTCTCTCTCTCAACCCCATACCAGCCTCTGTGCCAGCGACAGTCCTTCCAAATGGAGGGAGTGAAAT 1791

CCTTTGGTTTAATTATTTTCTCCTTCAAGGCACGCCTGCCACTAAGGTCAGGCTGACTTGCATGTCCCTCTAACGTTCG 1870

TAGCAGTGTGGTGGACACTGTCTTCCACCGACTGCTTCAATACCTCTGAAAGCCAGTGCTCGGAGTGCAGTTCGTGTAA 1949

ATTAATTTGCAGGAAGTATACTTGGCTAATTGTAGGGCTAGGATTGTGAATGAAATTTGCAAAGTCGCTTAGCAACAAT 2028

GGAAAGCCTTTCTCAGTCACACCGAGAAGTCACAACCAAGCCAGGTTGTGTAGAGTACAGCTGTGACATACAGACAGAA 2107

GAAGGCTGGGCTGGATGTCAGGCCTCAGATGACGGTTTCAGGTGCCAGGAACTATTACCATTCTGTATCTATCCAGAGT 2186

TATTAAAATTGAAAGTTGCACACATTTGTATAAGCATGCCTTTCTCCTGAGTTTTAAATTATATGTATACACAAACATG 2265

TGGCCCTCAAAGATCATGCACAAACCACTACTCTTTGCTAATTCTTGGACTTTTCTCTTTGATTTTCAATAAATACAAA 2344

TCCCCTTCATGCAAAAAAAAAAAAAAAGGGCGGCCGC                                         2381
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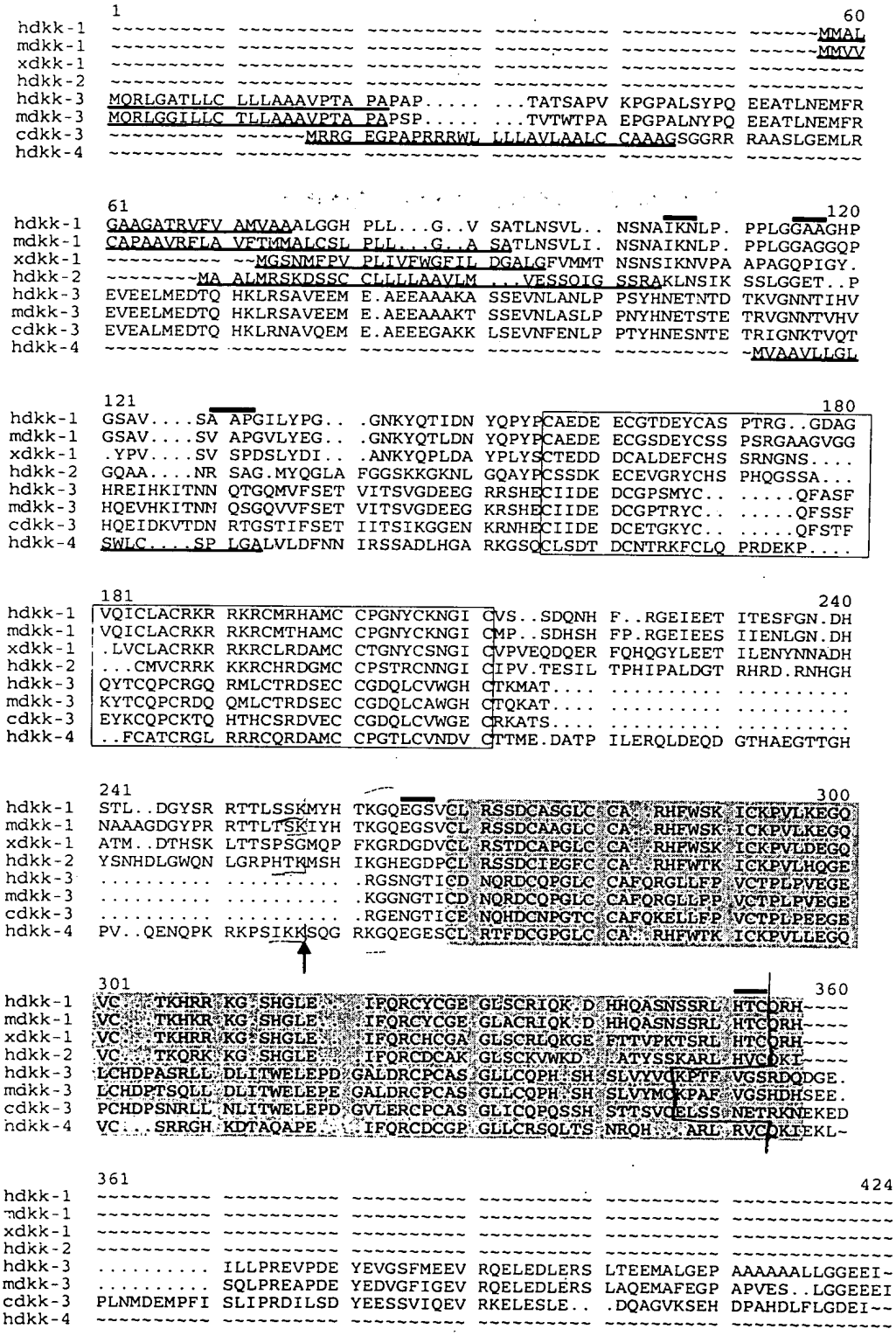
Figure 6


1 60
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mdkk-1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~MMVV
xdkk-1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
hdkk-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
hdkk-3 MQRLGATLLC LLLAAAVPTA PAPAP..... ...TATSAPV KPGPALSYPQ EEATLNEMFR
mdkk-3 MQRLGGILLC TLLAAAVPTA PAPSP..... ...TVTWTPA EPGPALNYPQ EEATLNEMFR
cdkk-3 ~~~~~~~~~~ ~~~~~~MRRG EGPAPRRRWL LLLAVLAALC CAAAGSGGRR RAASLGEMLR
hdkk-4 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
61 120
hdkk-1 GAAGATRVFV AMVAAALGGH PLL...G..V SATLNSVL.. NSNAIKNLP. PPLGGAAGHP
mdkk-1 CAPAAVRFLA VFTMMALCSL PLL...G..A SATLNSVLI. NSNAIKNLP. PPLGGAGGQP
xdkk-1 ~~~~~~~~~~ ~~MGSNMFPV PLIVFWGFIL DGALGFVMMT NSNSIKNVPA APAGQPIGY.
hdkk-2 ~~~~~~~~MA ALMRSKDSSC CLLLLAAVLM ...VESSQIG SSRAKLNSIK SSLGGET..P
hdkk-3 EVEELMEDTQ HKLRSAVEEM E.AEEAAAKA SSEVNLANLP PSYHNETNTD TKVGNNTIHV
mdkk-3 EVEELMEDTQ HKLRSAVEEM E.AEEAAAKT SSEVNLASLP PNYHNETSTE TRVGNNTVHV
cdkk-3 EVEALMEDTQ HKLRNAVQEM E.AEEEGAKK LSEVNFENLP PTYHNESNTE TRIGNKTVQT
hdkk-4 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~MVAAVLLGL
121 180
hdkk-1 GSAV....SA APGILYPG.. .GNKYQTIDN YQPYPCAEDE ECGTDEYCAS PTRG..GDAG
mdkk-1 GSAV....SV APGVLYEG.. .GNKYQTLDN YQPYPCAEDE ECGSDEYCSS PSRGAAGVGG
xdkk-1 .YPV....SV SPDSLYDI.. .ANKYQPLDA YPLYSCTEDD DCALDEFCHS SRNGNS....
hdkk-2 GQAA....NR SAG.MYQGLA FGGSKKGKNL GQAYPCSSDK ECEVGRYCHS PHQGSSA...
hdkk-3 HREIHKITNN QTGQMVFSET VITSVGDEEG RRSHECIIDE DCGPSMYC.. .....QFASF
mdkk-3 HQEVHKITNN QSGQVVFSET VITSVGDEEG KRSHECIIDE DCGPTRYC.. .....QFSSF
cdkk-3 HQEIDKVTDN RTGSTIFSET IITSIKGGEN KRNHECIIDE DCETGKYC.. .....QFSTF
hdkk-4 SWLC....SP LGALVLDFNN IRSSADLHGA RKGSQCLSDT DCNTRKFCLQ PRDEKP....
181 240
hdkk-1 VQICLACRKR RKRCMRHAMC CPGNYCKNGI CVS..SDQNH F..RGEIEET ITESFGN.DH
mdkk-1 VQICLACRKR RKRCMTHAMC CPGNYCKNGI CMP..SDHSH FP.RGEIEES IIENLGN.DH
xdkk-1 .LVCLACRKR RKRCLRDAMC CTGNYCSNGI CVPVEQDQER FQHQGYLEET ILENYNNADH
hdkk-2 ...CMVCRRK KKRCHRDGMC CPSTRCNNGI CIPV.TESIL TPHIPALDGT RHRD.RNHGH
hdkk-3 QYTCQPCRGQ RMLCTRDSEC CGDQLCVWGH CTKMAT.... ....
mdkk-3 KYTCQPCRDQ QMLCTRDSEC CGDQLCAWGH CTQKAT.... ....
cdkk-3 EYKCQPCKTQ HTHCSRDVEC CGDQLCVWGE CRKATS.... ....
hdkk-4 ..FCATCRGL RRRCQRDAMC CPGTLCVNDV CTTME.DATP ILERQLDEQD GTHAEGTTGH
241 300
hdkk-1 STL..DGYSR RTTLSSKMYH TKGQEGSVCL RSSDCASGLC CA..RHFWSK ICKPVLKEGQ
mdkk-1 NAAAGDGYPR RTTLTSKIYH TKGQEGSVCL RSSDCAAGLC CA..RHFWSK ICKPVLKEGQ
xdkk-1 ATM..DTHSK LTTSPSGMQP FKGRDGDVCL RSTDCAPGLC CA..RHFWSK ICKPVLDEGQ
hdkk-2 YSNHDLGWQN LGRPHTKMSH IKGHEGDPCL RSSDCIEGFC CA..RHFWTK ICKPVLHQGE
hdkk-3 .... .RGSNGTICD NQRDCQPGLC CAFQRGLLFP VCTPLPVEGE
mdkk-3 .... .KGGNGTICD NQRDCQPGLC CAFQRGLLPP VCTPLPVEGE
cdkk-3 .... .RGENGTICE NQHDCNPGTC CAFQKELLFP VCTPLPEEGE
hdkk-4 PV..QENQPK RKPSIKKSQG RKGQEGESCL RTFDCGPGLC CA..RHFWTK ICKPVLLEGQ
301 360
hdkk-1 VC..TKHRR KG SHGLE..IFQRCYCGE GLSCRIQK D HHQASNSSRL HTCQRH~~~~
mdkk-1 VC..TKHKR KG SHGLE..IFQRCYCGE GLACRIQK D HHQASNSSRL HTCQRH~~~~
xdkk-1 VC..TKHRR KG SHGLE..IFQRCHCGA GLSCRLQKGE FTTVPKTSRL HTCQRH~~~~
hdkk-2 VC..TKQRK KG SHGLE..IFQRCDCAK GLSCKVWKD. ATYSSKARL HVCQKI~~~~
hdkk-3 LCHDPASRLL DLITWELEPD GALDRCPCAS GLLCQPH SH SLVYVQKPTF VGSRDQDGE.
mdkk-3 LCHDPTSQLL DLITWELEPE GALDRCPCAS GLLCQPH SH SLVYMQKPAF VGSHDHSEE.
cdkk-3 PCHDPSNRLL NLITWELEPD GVLERCPCAS GLICQPQSSH STTSVQELSS NETRKNEKED
hdkk-4 VC...SRRGH KDTAQAPE..IFQRCDCGP GLLCRSQLTS NRQH..ARL RVCQKIEKL~
361 424
hdkk-1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
mdkk-1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
xdkk-1 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
hdkk-2 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
hdkk-3 .... ILLPREVPDE YEVGSFMEEV RQELEDLERS LTEEMALGEP AAAAAALLGGEEI~
mdkk-3 .... SQLPREAPDE YEDVGFIGEV RQELEDLERS LAQEMAFEGP APVES..LGGEEEI
cdkk-3 PLNMDEMPFI SLIPRDILSD YEESSVIQEV RKELESLE.. .DQAGVKSEH DPAHDLFLGDEI~~
hdkk-4 ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~

Figure 7

```
                                                                                  M     1
CTCGAGGCCAAAATTCGGCACGAGGCCGGGCTGTGGTCTAGCATAAAGGCGGAGCCCAGAAGAAGGGGCGGGGT ATG    77

 G   E   A   S   P   P   A   P   A   R   R   H   L   L   V   L   L   L   L   L     21
GGA GAA GCC TCC CCA CCT GCC CCC GCA AGG CGG CAT CTG CTG GTC CTG CTG CTG CTC CTC   137

 S   T   L   V   I   P   S   A   A   A   P   I   H   D   A   D   A   Q   E   S     41
TCT ACC CTG GTG ATC CCC TCC GCT GCA GCT CCT ATC CAT GAT GCT GAC GCC CAA GAG AGC   197

 S   L   G   L   T   G   L   Q   S   L   L   Q   G   F   S   R   L   F   L   K     61
TCC TTG GGT CTC ACA GGC CTC CAG AGC CTA CTC CAA GGC TTC AGC CGA CTT TTC CTG AAA   257

 G   N   L   L   R   G   I   D   S   L   F   S   A   P   M   D   F   R   G   L     81
GGT AAC CTG CTT CGG GGC ATA GAC AGC TTA TTC TCT GCC CCC ATG GAC TTC CGG GGC CTC   317

 P   G   N   Y   H   K   E   E   N   Q   E   H   Q   L   G   N   N   T   L   S    101
CCT GGG AAC TAC CAC AAA GAG GAG AAC CAG GAG CAC CAG CTG GGG AAC AAC ACC CTC TCC   377

 S   H   L   Q   I   D   K   M   T   D   N   K   T   G   E   V   L   I   S   E    121
AGC CAC CTC CAG ATC GAC AAG ATG ACC GAC AAC AAG ACA GGA GAG GTG CTG ATC TCC GAG   437

 N   V   V   A   S   I   Q   P   A   E   G   S   F   E   G   D   L   K   V   P    141
AAT GTG GTG GCA TCC ATT CAA CCA GCG GAG GGG AGC TTC GAG GGT GAT TTG AAG GTA CCC   497

 R   M   E   E   K   E   A   L   V   P   I   Q   K   A   T   D   S   F   H   T    161
AGG ATG GAG GAG AAG GAG GCC CTG GTA CCC ATC CAG AAG GCC ACG GAC AGC TTC CAC ACA   557

 E   L   H   P   R   V   A   F   W   I   I   K   L   P   R   R   R   S   H   Q    181
GAA CTC CAT CCC CGG GTG GCC TTC TGG ATC ATT AAG CTG CCA CGG CGG AGG TCC CAC CAG   617

 D   A   L   E   G   G   H   W   L   S   E   K   R   H   R   L   Q   A   I   R    201
GAT GCC CTG GAG GGC GGC CAC TGG CTC AGC GAG AAG CGA CAC CGC CTG CAG GCC ATC CGG   677

 D   G   L   R   K   G   T   H   K   D   V   L   E   E   G   T   E   S   S   S    221
GAT GGA CTC CGC AAG GGG ACC CAC AAG GAC GTC CTA GAA GAG GGG ACC GAG AGC TCC TCC   737

 H   S   R   L   S   P   R   K   T   H   L   L   Y   I   L   R   P   S   R   Q    241
CAC TCC AGG CTG TCC CCC CGA AAG ACC CAC TTA CTG TAC ATC CTC AGG CCC TCT CGG CAG   797

 L   *                                                                            243
CTG TAG                                                                           803

GGGTGGGGACCGGGGAGCACCTGCCTGTAGCCCCCATCAGACCCTGCCCCAAGCACCATATGGAAATAAAGTTCTTTCT   882

TACATCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTGGCGGCCGC                                   928
```

Figure 8

```
                                                                       M   C   R   L   R         5
GAATTCGGCACGAGGCAGAAGGCGCGAATGAAGGCAAAGCCTCCCACCCACCTGCA ATG TGT CGA CTG AGG        71

 V   L   L   L   L   L   P   L   A   F   V   S   S   S   A   L   P   I   H   D      25
GTC TTG CTG CTG CTG CTC CCC TTG GCC TTC GTG TCC TCC TCT GCT CTC CCC ATC CAT GAT    131

 V   D   S   Q   Q   N   T   S   G   F   L   G   L   Q   R   L   L   Q   S   F      45
GTC GAC TCT CAG CAG AAC ACC TCC GGG TTC CTG GGC CTT CAG AGG CTT CTC CAA AGC TTT    161

 S   R   L   F   L   K   N   D   L   L   R   D   L   D   N   F   F   S   S   P      65
AGT CGA CTG TTC CTA AAA AAT GAC CTG CTA CGA GAC CTG GAC AAC TTC TTC TCC TCC CCC    251

 M   D   F   R   D   L   P   R   N   F   H   Q   E   E   N   Q   E   H   R   M      85
ATG GAC TTC CGA GAC CTT CCT AGG AAC TTC CAT CAG GAA GAG AAC CAG GAG CAC AGA ATG    311

 G   N   H   T   L   S   S   H   L   Q   I   D   K   V   T   D   N   Q   T   G     105
GGC AAC CAT ACC CTC TCC AGC CAC CTA CAG ATA GAC AAG GTG ACT GAC AAC CAG ACA GGG    371

 E   V   H   I   S   E   K   V   E   A   S   I   E   P   E   R   N   P   E   G     125
GAG GTG CAC ATC TCG GAG AAA GTC GAG GCC TCC ATT GAG CCA GAA CGG AAC CCG GAA GGG    431

 D   W   K   V   P   K   V   E   A   K   E   P   P   V   P   V   Q   K   V   T     145
GAC TGG AAG GTT CCC AAA GTA GAA GCA AAA GAG CCC CCG GTG CCT GTG CAG AAG GTC ACC    491

 D   S   L   H   P   E   P   R   Q   V   A   F   W   I   M   K   M   P   R   R     165
GAC AGC TTG CAC CCA GAG CCC CGG CAG GTG GCT TTC TGG ATC ATG AAG ATG CCA AGG CGG    551

 R   T   Q   P   D   V   Q   D   G   G   R   W   L   I   E   K   R   H   R   M     185
AGG ACC CAG CCC GAT GTC CAG GAT GGA GGC CGC TGG CTC ATA GAA AAG CGA CAT CGC ATG    611

 Q   A   I   R   D   G   L   R   G   G   A   R   E   D   S   L   E   D   G   V     205
CAG GCC ATC CGG GAT GGG CTC CGT GGA GGC GCC CGT GAG GAC AGC CTG GAG GAT GGG GTC    671

 H   I   P   Q   H   A   K   L   P   V   R   K   T   H   F   L   Y   I   L   R     225
CAT ATC CCC CAA CAC GCC AAG CTG CCT GTC AGA AAG ACA CAC TTT CTC TAC ATC CTC AGG    731

 P   S   Q   Q   L   *                                                             231
CCA TCC CAA CAG CTG TAA GTGGGGACCAGATGTCCCACACCCTACCCCAACACCATATGGAAATAAAGGTTTTC    805

TTACATCTAAAAAAAAAAAAAAAAAAAAA                                                      835
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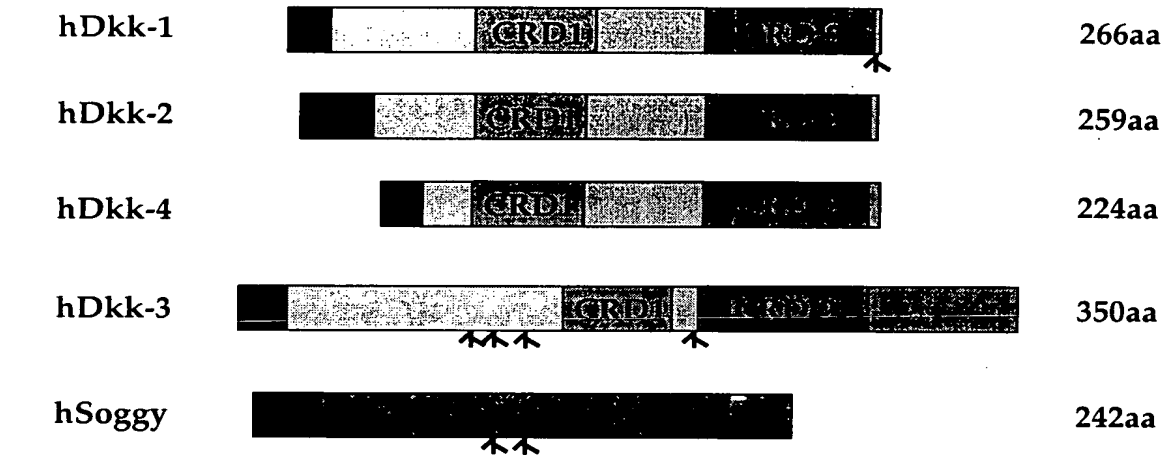
Figure 9

A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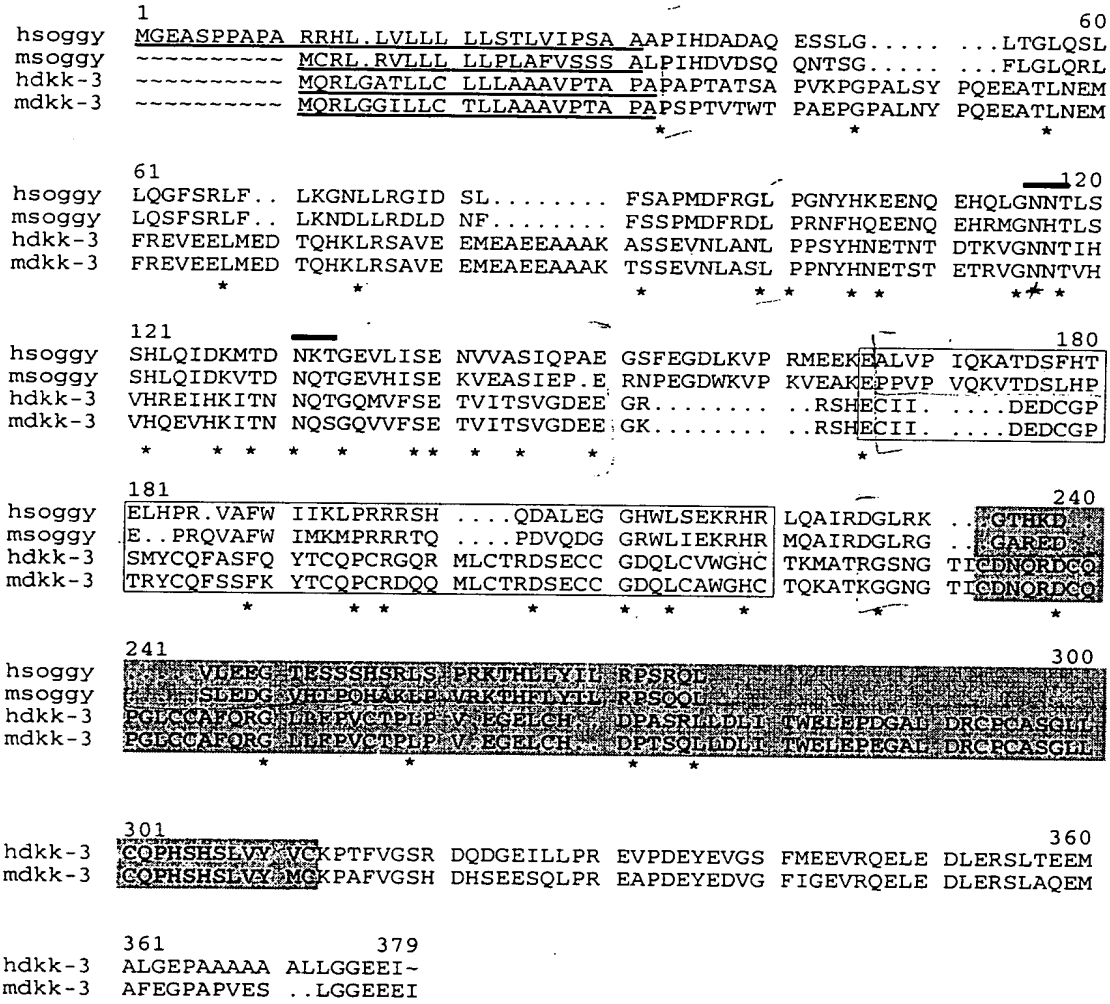
CRD1
266aa
hDkk-2
CRD1
259aa
hDkk-4
CRD1
224aa
hDkk-3
CRD1
350aa
hSoggy
242aa

Figure 10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msoggy ~~~~~~~~~~ MCRL.RVLLL LLPLAFVSSS ALPIHDVDSQ QNTSG..... ...FLGLQRL
hdkk-3 ~~~~~~~~~~ MQRLGATLLC LLLAAAVPTA PAPAPTATSA PVKPGPALSY PQEEATLNEM
mdkk-3 ~~~~~~~~~~ MQRLGGILLC TLLAAAVPTA PAPSPTVTWT PAEPGPALNY PQEEATLNEM
hsoggy LQGFSRLF.. LKGNLLRGID SL..... FSAPMDFRGL PGNYHKEENQ EHQLGNNTLS
msoggy LQSFSRLF.. LKNDLLRDLD NF..... FSSPMDFRDL PRNFHQEENQ EHRMGNHTLS
hdkk-3 FREVEELMED TQHKLRSAVE EMEAEEAAAK ASSEVNLANL PPSYHNETNT DTKVGNNTIH
mdkk-3 FREVEELMED TQHKLRSAVE EMEAEEAAAK TSSEVNLASL PPNYHNETST ETRVGNNTVH
hsoggy SHLQIDKMTD NKTGEVLISE NVVASIQPAE GSFEGDLKVP RMEEKEALVP IQKATDSFHT
msoggy SHLQIDKVTD NQTGEVHISE KVEASIEP.E RNPEGDWKVP KVEAKEPPVP VQKVTDSLHP
hdkk-3 VHREIHKITN NQTGQMVFSE TVITSVGDEE GR..... ..RSHECII. ....DEDCGP
mdkk-3 VHQEVHKITN NQSGQVVFSE TVITSVGDEE GK..... ..RSHECII. ....DEDCGP
hsoggy ELHPR.VAFW IIKLPRRRSH ....QDALEG GHWLSEKRHR LQAIRDGLRK ..GTHKD
msoggy E..PRQVAFW IMKMPRRRTQ ....PDVQDG GRWLIEKRHR MQAIRDGLRG ..GARED
hdkk-3 SMYCQFASFQ YTCQPCRGQR MLCTRDSECC GDQLCVWGHC TKMATRGSNG TICDNQRDCQ
mdkk-3 TRYCQFSSFK YTCQPCRDQQ MLCTRDSECC GDQLCAWGHC TQKATKGGNG TICDNQRDCQ
hsoggy VLEEG TESSSHSRLS PRKTHLLYIL RPSRQL
msoggy SLEDG VHTPQHAKLP VRKTHTLYIL RPSQQL
hdkk-3 PGLCCAFQRG LLRPVCTPLP VEGELCH DPASRLLDLI TWELEPDGAL DRCPCASGLL
mdkk-3 PGLGCAFQRG LLRPVCTPLP VEGELCH DPTSQLLDLI TWELEPEGAL DRCPCASGLL
hdkk-3 CQPHSHSLVY VCKPTFVGSR DQDGEILLPR EVPDEYEVGS FMEEVRQELE DLERSLTEEM
mdkk-3 CQPHSHSLVY MCKPAFVGSH DHSEESQLPR EAPDEYEDVG FIGEVRQELE DLERSLAQEM
hdkk-3 ALGEPAAAAA ALLGGEEI~
mdkk-3 AFEGPAPVES ..LGGEEEI

Figure 11

```
          1                                                                                                       100
hDkk-1    TKGQEGSVCL RSSDCASGLC CA..RHFWSK ICKPVLKEGQ VCTKHRRK.. .....GSHGL EIFQRCYCGE GLSCRIQKDH HQASNSSRLH TCQRH~~~~~
hDkk-2    IKGHEGDPCL RSSDCIEGFC CA..RHFWTK ICKPVLHQGE VCTKQRKK.. .....GSHGL EIFQRCDCAK GLSCKVWKD. ATYSSKARLH VCQKI~~~~~
hDkk-3    TRGSNGTICD NQRDCQPGLC CAFQRGLLFP VCTPLPVEGE LCHDPASRLL DLITWELEPD GALDRCPCAS GLLC...... .QPHSHSLVY VCKPTFVGSR
hDkk-4    RKGQEGESCL RTFDCGPGLC CA..RHFWTK ICKPVLLEGQ VCSRRGHK.. ....DTAQAP EIFQRCDCGP GLLCRSQLTS NR..QHARLR VCQKIEKL~~
colipase  INLENGELCM NSAQCKSN.C CQHSSALGLA RCTSMASENS ECSVKTL... .........Y GIYYKCPCER GLTCEGDKTI VGSITNTNFG ICHDAGRSKQ
              G C         C     C C           C             C                             C C      GL C                 C
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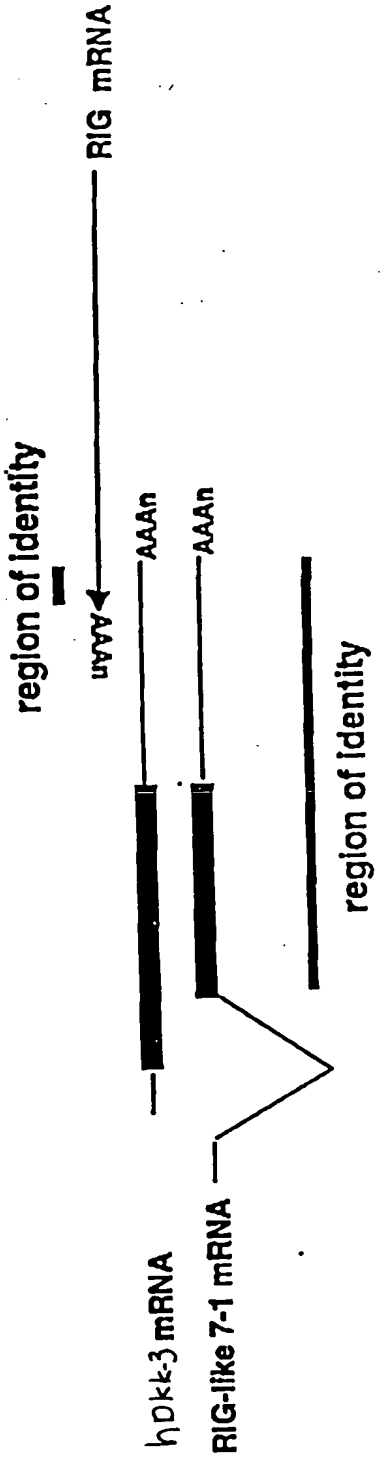
Figure 12


RIG mRNA
region of identity
AAAn
AAAn
AAAn
region of identity
hDkk-3 mRNA
RIG-like 7-1 mRNA